

Strain	Source	Year	Isolation	Characteristics	References
101	Human	1964	17	First isolate	1
102	Human	1964	18	First isolate	1
103	Human	1964	19	First isolate	1
104	Human	1964	20	First isolate	1
105	Human	1964	21	First isolate	1
106	Human	1964	22	First isolate	1
107	Human	1964	23	First isolate	1
108	Human	1964	24	First isolate	1
109	Human	1964	25	First isolate	1
110	Human	1964	26	First isolate	1
111	Human	1964	27	First isolate	1
112	Human	1964	28	First isolate	1
113	Human	1964	29	First isolate	1
114	Human	1964	30	First isolate	1
115	Human	1964	31	First isolate	1
116	Human	1964	32	First isolate	1
117	Human	1964	33	First isolate	1
118	Human	1964	34	First isolate	1
119	Human	1964	35	First isolate	1
120	Human	1964	36	First isolate	1
121	Human	1964	37	First isolate	1
122	Human	1964	38	First isolate	1
123	Human	1964	39	First isolate	1
124	Human	1964	40	First isolate	1
125	Human	1964	41	First isolate	1
126	Human	1964	42	First isolate	1
127	Human	1964	43	First isolate	1
128	Human	1964	44	First isolate	1
129	Human	1964	45	First isolate	1
130	Human	1964	46	First isolate	1
131	Human	1964	47	First isolate	1
132	Human	1964	48	First isolate	1
133	Human	1964	49	First isolate	1
134	Human	1964	50	First isolate	1
135	Human	1964	51	First isolate	1
136	Human	1964	52	First isolate	1
137	Human	1964	53	First isolate	1
138	Human	1964	54	First isolate	1
139	Human	1964	55	First isolate	1
140	Human	1964	56	First isolate	1
141	Human	1964	57	First isolate	1
142	Human	1964	58	First isolate	1
143	Human	1964	59	First isolate	1
144	Human	1964	60	First isolate	1
145	Human	1964	61	First isolate	1
146	Human	1964	62	First isolate	1
147	Human	1964	63	First isolate	1
148	Human	1964	64	First isolate	1
149	Human	1964	65	First isolate	1
150	Human	1964	66	First isolate	1
151	Human	1964	67	First isolate	1
152	Human	1964	68	First isolate	1
153	Human	1964	69	First isolate	1
154	Human	1964	70	First isolate	1
155	Human	1964	71	First isolate	1
156	Human	1964	72	First isolate	1
157	Human	1964	73	First isolate	1
158	Human	1964	74	First isolate	1
159	Human	1964	75	First isolate	1
160	Human	1964	76	First isolate	1
161	Human	1964	77	First isolate	1
162	Human	1964	78	First isolate	1
163	Human	1964	79	First isolate	1
164	Human	1964	80	First isolate	1
165	Human	1964	81	First isolate	1
166	Human	1964	82	First isolate	1
167	Human	1964	83	First isolate	1
168	Human	1964	84	First isolate	1
169	Human	1964	85	First isolate	1
170	Human	1964	86	First isolate	1
171	Human	1964	87	First isolate	1
172	Human	1964	88	First isolate	1

1. SUBUNIT A (CEFA/1 FIMBRIAL) ARE RATHER RIGHT, THIRGAL LINE 117 (AMINO ACID
 2. 95) IS INTERESTING, WITH AN APPEARING AXIAL DUE, AND A DIAMETER OF
 3. 2. NANOMETERS. A SINGLE CEFA/1 FIMBRIA CONSISTS OF APPROX 100
 4. IDENTICAL PROTEIN SUBUNIT.
 5. 1. INDUCTION OF CEFA/1 FIMBRIAL ARE ONLY EXPRESSED IN THE PRESENCE OF
 6. THE POSITIVE REGULATOR CPAD.
 7. 1. SIMILARITY TO THE CE1 FIMBRIAL SUBUNIT A (CEFA)
 8. THIS SWISS PROTEIN ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION
 9. BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION
 10. THE BIOGRAPHIC BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
 11. USE BY ANY PROTEIN INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
 12. MODIFIED AND THIS STATEMENT IS NOT REMOVED. ISSUED BY AND FOR COMBIORETAIL
 13. OUTSTATIONS REQUIRES A LICENSE AGREEMENT (See <http://www.ebi.ac.uk/annotation/>
 14. OF SEND AN EMAIL TO biocomp@ebi.ac.uk).
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Query Match 72.0% Score 36: PB 1: Length 244:
 Best Local Similarity 60.0%: Prol. No. 6.5:
 Matches 6: Conservative 4: Mismatches 1: Indels 0: Gaps 0:

QY 1 PSAVALITYSP 10
 1 1 1 1 1 1 1
 Db 84 PNASALITYSP 93

RESULT 4
 MTC2.CHVP1 STANDARD: PRT: 326 AA.
 AC P41118: Q84569;
 DI 01-JUL-1993 (Ref. 26, Created)
 DI 15-DEC-1998 (Ref. 37, Last sequence update)
 DI 20-AUG-2001 (Ref. 40, Last annotation update)
 DE MODIFICATION METHYLASE CVIALL (EC 2.1.1.72) (ADENINE SPECIFIC METHYLTRANSFERASE CVIALL) (M.CVIALL).
 DE CVIATIM OR A25LR.
 DE Paracetamum bacteriophage chlorofila virus 1 (PhV-1).
 DE Viruses: dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.
 DE NCBI TaxID: 10506;
 RX MEDLINE: 93065201; PubMed 1437552;
 RA Zhang Y., Nelson M., Nucleotide J.W., Fairbank D.P., van Etten J.L.;
 RT "Characterization of Chlorofila virus PhV-1 CVIALL restriction and modification system."
 RT Nucleic Acids Res. 20:5351-5356(1992).
 RN 121
 RP REVISIONS. AND SEQUENCE FROM N.A.
 RA MEDLINE: 95133167; PubMed 7831789;
 RA Lu Z., Li Y., Zhang Y., Kishish G.F., Rock D.L., van Etten J.L.;
 RT "Analysis of 45 kb of DNA located at the left end of the chlorofila virus PhV-1 genome."
 RT Virology 206:339-352(1995).
 CC -1- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CATG, CAUSES SPECIFIC METHYLATION ON A-2 ON BOTH STRANDS AND PROTECTS THE DNA FROM CLEAVAGE BY THE CVIALL END-NUCLEASE.
 CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA ADENINE -> S-ADENOSYL-L-HOMOCYSTEINE + DNA 6-METHYLAMINOURINE.
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DR EMBL: M86639; AAB92181.1;
 DR EMBL: 042580; AAC96619.1;
 DR PIR: S27901; S27901.
 DR PIR: S25442; S25442.
 DR REFSEQ: J5422; M.CVIALL.
 DR InterPro: IPR002294; D12N6.mltase.
 DR InterPro: IPR002052; No_MLase.
 DR Pfam: PF02086; Methyltransf12.1.
 DR PRINTS: PF00505; D12N6M.LTASE.
 DR PROSITE: PS00092; No_MLASE.1.
 KW Transposase; Methyltransferase; Restriction system.
 SO SEQUENCE 126 AA; 37492 MW; 80C16750B540094 CRC64;

Query Match 72.0% Score 36: PB 1: Length 126:
 Best Local Similarity 70.0%: Prol. No. 9.3:
 Matches 7: Conservative 0: Mismatches 4: Indels 0: Gaps 0:

QY 1 PSAVALITYSP 10
 1 1 1 1 1 1 1
 Db 95 PNASALITYSP 104

RESULT 5
 VMA1_P12H1 STANDARD: PRT: 477 AA.
 ID VMA1_P12H1
 AC P24266;
 DI 01-MAR-1992 (Ref. 21, Created)
 DI 01-MAR-1992 (Ref. 21, Last sequence update)
 DI 01-AUG-1992 (Ref. 24, Last annotation update)
 DE MATRIX PROTEIN (MEMBRANE PROTEIN).
 DE M.
 DE Human parainfluenza 2 virus (strain Jishiba) (PIV 2).
 DE Viruses: ssRNA negative-strand viruses; Mononegavirales;
 DE Paramyxoviridae; Paramyxovirinae; Rubulaviruses.
 DE NCBI TaxID: 11214;
 RX MEDLINE: 9109454; PubMed 2174264;
 RA Kawano M., Bando H., Ohamoto S., Okamoto K., Kondo K., Imai et al. M.;
 RA Nishio M., Ito Y.;
 RT "Complete nucleotide sequence of the matrix gene of human parainfluenza type 2 virus and expression of the M protein in bacteria."
 RT Virology 179:857-861(1990).
 CC -1- FUNCTION: THE M PROTEIN HAS A CROCIAT. ROLE IN VIRUS ASSEMBLY AND INTERAITS WITH THE RNP COMPLEX AS WELL AS WITH THE VIRAL MEMBRANE.
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DR EMBL: M62734; AAA4662.1;
 DR EMBL: X57559; CAA40785.1;
 DR PIR: A46421; MENV2.
 DR PIR: S16661; S16661.
 DR InterPro: IPR000982; Matrix.
 DR Pfam: PF00661; Matrix.1.
 DR PROSITE: PRO0741; Matrix.1.
 KW Matrix protein; Envelope protein.
 SO SEQUENCE 477 AA; 42412 MW; A181A79C55276746 CRC64;

Query Match 72.0% Score 36: PB 1: Length 477:
 Best Local Similarity 60.0%: Prol. No. 11:
 Matches 6: Conservative 4: Mismatches 1: Indels 0: Gaps 0:

QY 1 PSAVALITYSP 10
 1 1 1 1 1 1 1
 Db 170 PNASALITYSP 179

RESULT 6
 PGLN_RHV1 STANDARD: PRT: 244 AA.
 ID PGLN_RHV1
 AC P27410;
 DI 01-AUG-1992 (Ref. 23, Created)
 DI 01-AUG-1992 (Ref. 23, Last sequence update)
 DI 20-AUG-2001 (Ref. 40, Last annotation update)
 DE NON-STRUCTURAL POLYPEPTIDE CONTAINING RNA-DIRECTED RNA POLYMERASE (NS 2.7.7.48); (HIV-1 PROTEASE P20 (EC 3.4.22.)) HELICASE (EC 3.6.1.1)
 DE Rabbit hemorrhagic disease virus (RHDV).
 DE Viruses: ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 DE Caliciviruses.
 DE NCBI TaxID: 11976;
 RX MEDLINE: 9101557; PubMed 1840711;
 RX MEDLINE: 9101557; PubMed 1840711;

[13]
 RP MEDLINE=87051757; PubMed=4096579;
 RA Schib R., Atcher W., Gall U., Goto S., Preiss A., Muto T.,
 RA Seifert E., Nuber U., Schroeder G., Komler R., Jackle H.;
 RT *A conserved family of nuclear proteins containing structural
 RT elements of the finger protein encoded by Kruppel, a Drosophila
 RT segmentation gene.*
 RL Cell 47:1025-1032(1996).
 CC -1- FUNCTION: PLAYS A GENERAL ROLE IN THE HIERARCHIES OF GENE
 CC EXPRESSION LEADING TO METAMORPHOSIS.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA AND BETA (SHOWN HERE); ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DEVELOPMENTAL STAGE: BETA ISOFORM IS EXPRESSED DURING
 CC EMBRYOGENESIS, MOST ABUNDANT IN MIDEKRYOTINESIS, AND IN ADULTS.
 CC ALPHA ISOFORM IS EXPRESSED FROM EMBRYOGENESIS TO 8 HOURS AFTER
 CC POPULATION. MAJOR PERIOD OF EXPRESSION IS DURING SECOND INSTAR.
 CC -1- SIMILARITY: BELONGS TO THE KROEPEL FAMILY OF C2H2 TYPE ZINC-
 CC FINGER PROTEINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AJ005440; GAO6543.2;
 DR EMBL: AJ005441; GAO6544.2;
 DR EMBL: AF003612; AAF52434.2;
 DR EMBL: AF003612; AAG22417.1;
 DR EMBL: M14940; AAA28660.1;
 DR HSSP: P08047; 1SP2;
 DR Flybase: FBgn0028420; K1-b1.
 DR InterPro: IPR000822; Znf-C2H2.
 DR Pfam: PF00096; Zf-C2H2; 10.
 DR SMART: SM00355; Znf_C2H2; 8.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 8.
 DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 2.
 DR K1: PROSITE: PS00157; ZINC_FINGER_C2H2_2; 2.
 KW Zinc-finger; Metal-binding; DNA-binding; Repeat; Alternative splicing;
 KW Developmental protein.
 FT DOMAIN 108 148 QIN_RICH
 FT DOMAIN 482 515 SER/THR-RICH
 FT DOMAIN 538 565 SER/THR-RICH
 FT DOMAIN 194 463 ZINC_FINGERS
 FT ZN_FING 194 216 C2H2-TYPE
 FT ZN_FING 271 293 C2H2-TYPE
 FT ZN_FING 299 321 C2H2-TYPE
 FT ZN_FING 327 349 C2H2-TYPE
 FT ZN_FING 355 477 C2H2-TYPE
 FT ZN_FING 383 407 C2H2-TYPE
 FT ZN_FING 413 435 C2H2-TYPE
 FT ZN_FING 441 463 C2H2-TYPE
 FT VARSPLIT 1 54 MISSING (IN ISOFORM ALPHA).
 FT CONFLICT 313 413 N vs D (IN REF. 3).
 SO SEQUENCE 845 AA; 91451 MW; A41878968P4E4372 C6764;

01 JAN 1990 (Ref. 13, last sequence update)
 02 MAY-2000 (Ref. 39, last annotation update)
 03 CHITIN SYNTHASE 2 (P02411b) (CHITIN-UDP ACETYL-GLUCOSAMINE
 04 TRANSFERASE 2).
 05 CHS2 OR YBR068W OR YBR0407.
 06 Saccharomyces cerevisiae (baker's yeast).
 07 Eukaryotic. Euk: Ascomycota: Saccharomycotina: Saccharomycetes.
 08 Saccharomycetiales: Saccharomycetaceae: Saccharomyces
 09 NMLTAXID: 4942.
 10 [1]
 11 SEQUENCE FROM N.A.
 12 MEDLINE 9014137; PubMed 2534406;
 13 Silverman S.J.;
 14 *Similar and different domains of chitin synthases 1 and 2 of S.
 15 cerevisiae: two isozymes with distinct functions.*
 16 Yeast 5:459-467(1989).
 17 [2]
 18 SEQUENCE FROM N.A.
 19 Andre B., Grolleuch C., Hehn G., Jaudoux J.C., Drouotard A.,
 20 Vissers S.;
 21 Submitted (Aug-1994) to the EMBL/GenBank/DDBJ databases.
 22 [3]
 23 MUTAGENESIS.
 24 MEDLINE 95294998; PubMed 7775457;
 25 Nishishiki S., Sudoh M., Uno N., Sawada R., Yamaguchi E., Ishida Y.,
 26 Moto T., Takai M., Arisawa M., Yamada-Okae H.;
 27 *Characterization of chitin synthase 2 of Saccharomyces cerevisiae.
 28 Implication of two highly conserved domains as possible catalytic
 29 sites.*
 30 J. Biol. Chem. 270:13961-13967(1995).
 31 [4]
 32 IS REQUIRED FOR MAINTAINING NORMAL CHL. MEMBR. OR.
 33 -1- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + [1,4-(N-ACETYL-BETA-D-
 34 GLUCOSAMINYL)](n-1) -> UDP + [1,4-(N-ACETYL-BETA-D-
 35 GLUCOSAMINYL)](n).
 36 -1- ENZYME REGULATION: REQUIRES PROTEOLYTIC ACTIVATION.
 37 -1- SUBCELLULAR LOCATION: INTERNAL MEMBRANE PROTEIN.
 38 -1- SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY.
 39 [5]
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 46 or send an email to license@isb-sib.ch).
 47 -----
 DR EMBL: M24865; AAA34493.1;
 DR EMBL: Z35907; GAA84980.1;
 DR PIR: S45167; S45167.
 DR PIR: A10922; A10922.
 DR SCD: S0010242; CHS2.
 DR InterPro: IPR002923; Chitin_synth.
 DR InterPro: IPR001173; Glycosylase_2.
 DR Pfam: PF01644; Chitin_synth_1.
 DR PROSITE: PS002998; Chitin_Synth_1.
 KW Transferrase; glycosyltransferase; Cell wall;
 KW Multigene family;
 FT DOMAIN 1 422 EXTRA-CELLULAR (POTENTIAL)
 FT TRANSMEM 423 443 1 (POTENTIAL)
 FT TRANSMEM 444 643 CYTOPLASMIC (POTENTIAL)
 FT TRANSMEM 644 664 2 (POTENTIAL)
 FT TRANSMEM 665 677 EXTRA-CELLULAR (POTENTIAL)
 FT TRANSMEM 678 698 4 (POTENTIAL)
 FT TRANSMEM 699 711 CYTOPLASMIC (POTENTIAL)
 FT TRANSMEM 712 732 4 (POTENTIAL)
 FT TRANSMEM 733 743 EXTRA-CELLULAR (POTENTIAL)
 FT TRANSMEM 744 764 5 (POTENTIAL)
 FT TRANSMEM 765 775 CYTOPLASMIC (POTENTIAL)
 FT TRANSMEM 776 796 6 (POTENTIAL)
 FT TRANSMEM 797 875 EXTRA-CELLULAR (POTENTIAL)
 FT TRANSMEM 876 896 7 (POTENTIAL).

[illegible][illegible]

Query Match 68.0% Score 34: 10 1: Length 640
 Best Local Similarity 60.0% Prod. No. 49
 Matches 6: Conservative 2: Mismatches 2: Indels 0: Gaps 0

QY 1 PSAAVLVS 10
 1: 1:1
 2 PSIAVLVS 11

RESULT 13
 BL14_CAEEL STANDARD: PRI: 684 AA.
 AC P51559:
 DT 01-OCT-1996 (Ref. 34, Created)
 DT 01-OCT-1996 (Ref. 34, Last sequence update)
 DT 20-AUG-2001 (Ref. 40, Last annotation update)
 DE ENDOPEPTIDASE BL1-4 PRECURSOR (EC 3.4.21.1) (BLISTERASTIS A. B. AND D.)
 GN BL1-4.
 OS Caenorhabditis elegans.
 NC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 Rhabditidae; Pelecinidae; Caenorhabditis.
 NCBI_TaxID 6239;
 (1)
 RN SEQUENCE FROM N.A.
 RP STRAIN BRISTOL N2;
 RX MEDLINE:95293228; PubMed-7774814;
 RA Thacker C., Peters K.W., Strayko M., Rose A.M.;
 RT "The bl-4 locus of Caenorhabditis elegans encodes structurally
 distinct kex2/subtilisin-like endopeptidases essential for early
 development and adult morphology.";
 RI Genes Dev. 9:956-971(1995)
 CC -1- FUNCTION: MAY BE RESPONSIBLE FOR PROCESSING STRUCTURAL CITICLE
 CC COMPONENTS.
 CC -1- ALTERNATIVE PRODUCTS: FOUR FORMS SEEM TO BE PRODUCED AS A RESULT
 CC OF ALTERNATIVE SPLICING OF THE SAME GENE. THEY DIFFER IN THEIR C-
 CC TERMINALS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8. ALSO KNOWN AS THE
 CC SUBTILASE FAMILY. FURIN SUBFAMILY.

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CC EMBL: L29438; AAA98750.1; -;
 CC EMBL: L29439; AAA98751.1; -;
 CC EMBL: L29440; AAA98752.1; -;
 CC HSSP: P04072; ITCC;
 DR InterPro: IPR002884; P-domain;
 DR InterPro: IPR002099; Peptidase-S8.
 DR Pfam: PF01483; P: 1.
 DR Pfam: PF00082; Peptidase-S8; 1.
 DR PRINTS: PR00723; SUBTILISIN.
 DR ProDom: PD000717; P-domain; 1.
 DR ProSite: PS00146; SUBTILASE_ASF; 1.
 DR ProSite: PS00137; SUBTILASE_HIS; 1.
 DR ProSite: PS00138; SUBTILASE_SER; 1.
 DR Hydrolase: Serine protease; Glycoprotein; Calcium-binding; Zymogen;
 KM Transmembrane; Signal; Alternative splicing.
 FT SIGNAL 1 20 POTENTIAL.
 FT PROPEP 21 116 BY SIMILARITY.
 FT CHAIN 117 684 ENDOPEPTIDASE BL1-4.
 FT ACT_SITE 202 202 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 241 241 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 415 415 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT TRANSMEM 417 437 POTENTIAL.
 FT DOMAIN 438 684 CYTOSOLASMIC (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLYCANIC) (POTENTIAL).
 FT VARSPPLIC 651 684 GSSSTHSIDNIHRRYPKQRMNYTLFRR-SQLHRA - WHO

Query Match 68.0% Score 34: 10 1: Length 644
 Best Local Similarity 66.7% Prod. No. 51
 Matches 6: Conservative 2: Mismatches 2: Indels 0: Gaps 0

QY 1 PSAAVLVS 9
 1: 1:1
 2 PSIAVLVS 10

RESULT 14
 DVL2_MOUSE
 DT 01-MAY-2000 (Ref. 39, Created)
 DT 01-MAY-2000 (Ref. 39, Last sequence update)
 DT 20-AUG-2001 (Ref. 40, Last annotation update)
 DE SEGMENT POLARITY PROTEIN DISHEVELLED DVL 2 (DISHVELLED 2)
 DE (DSH HOMOLOG 2).
 GN DVL2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Eutelestina;
 CC Mammalia; Eutheria; Rodentia; Sciurodonta; Muridae; Mus.
 CC NCBI_TaxID 10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX STRAIN BALB/c; TISSUE Brain;
 RX MEDLINE:97042042; PubMed-8887314;
 RA Klingenstein J., Yang Y., Axelrod J.D., Reier D.R., Fournham N.,
 SA Sussman D.J.;
 RT "Conservation of dishevelled structure and function between Dros and
 RT Mech. Dev. 58:15-26(1996).
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY
 CC MEDIATED BY MULTIPLE WNT GENES.
 CC -1- SUBCELLULAR LOCATION: CYTOSOLASMIC (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: ENDOTHELIUM.
 CC -1- SIMILARITY: BELONGS TO THE DSH FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 DEP/DHR DOMAIN.

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 CC or send an email to license@isb.slb.ch).

CC EMBL: U24560; AA052827.1;
 CC HSSP: P31016; ITCC;
 DR MGD: MGI:156613; DVL2.
 DR InterPro: IPR001591; DEP.
 DR InterPro: IPR001598; DIX.
 DR InterPro: IPR004451; Dishevelled.
 DR Pfam: PF00610; DEP; 1.
 DR Pfam: PF02477; Dishevelled; 1.
 DR Pfam: PF06778; DIX; 1.
 DR Pfam: PF00595; DVL2; 1.
 DR SMART: SM00021; DAX; 1.

ITSDVPSARSSPDLISWKLSTVIGTNTCTPSASST
 AYKHLTOLLNKGSSSEKIVKQITQYLLDKTKMSSSP
 HTCKAVVETKSSLLDIDVDMPIYDHRVFSSITIV
 ADVESNVOAKTWRKIDTADYINAVKCTLSSSTV
 TADPMSCGKSGVKGSTGVKQVPSKSSWCTPSS
 KIPDILLDSKSSSGEDMEIVVSHLAAGTAVKRSI
 TRSNVYAPLACYNNTNAINCAHDEEDDEIVN-
 QIV (IN BLISTERASE C).
 DSGG (IN BLISTERASE B).
 MISSING (IN BLISTERASE F).
 HA54AC1ACPA77AI CPG647

CC	-1- SIMILARITY: TO OTHER SODIUM CHANNEL PROTEINS	
CC	-1- SIMILARITY: CONTAINS 1 TO DOMAIN	
CC	-1- DATABASE: NAME, LQTSdb; NOTE: SCNA mutations poster	
CC	WWW: http://www.ssi.dk/en/forskning/1qtsdb/scna.htm	
CC	-----	
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CC	entities requires a license agreement (see http://www.ebi.ac.uk/autonuce/	
CC	or send an email to license@ebi.ac.uk).	
CC	-----	
DR	EMBL: M7235; AA58644.1; -	
DR	MIM: 600163; -	
DR	InterPro: IPR002111; Cat_channel_Trip.	
DR	InterPro: IPR000636; Cat_channel_1q.	
DR	InterPro: IPR001682; Channel_pore_Ca_Na	
DR	InterPro: IPR000048; IQ.	
DR	InterPro: IPR001696; Na_channel.	
DR	Pfam: PF00520; Ion_trans_4.	
DR	Pfam: PF00612; IQ; 1.	
DR	PRINTS: PR00170; NACHANNEL.	
DR	SMART: SM00315; IQ; 1.	
KW	ionic channel; Transmembrane; Ion transport; Voltage-gated channel;	
KW	Glycoprotein; Repeat; Multigene family; Phosphorylation;	
KW	Polymorphism; Disease mutation; Long Q syndrome.	
FT	TRANSMEM 127 150	S1 OF REPEAT 1 (POTENTIAL).
FT	TRANSMEM 159 178	S2 OF REPEAT 1 (POTENTIAL).
FT	TRANSMEM 192 210	S3 OF REPEAT 1 (POTENTIAL).
FT	TRANSMEM 217 246	S4 OF REPEAT 1 (POTENTIAL).
FT	TRANSMEM 253 276	S5 OF REPEAT 1 (POTENTIAL).
FT	TRANSMEM 490 415	S6 OF REPEAT 1 (POTENTIAL).
FT	TRANSMEM 712 736	S1 OF REPEAT 11 (POTENTIAL).
FT	TRANSMEM 748 771	S2 OF REPEAT 11 (POTENTIAL).
FT	TRANSMEM 780 799	S3 OF REPEAT 11 (POTENTIAL).
FT	TRANSMEM 806 825	S4 OF REPEAT 11 (POTENTIAL).
FT	TRANSMEM 842 862	S5 OF REPEAT 11 (POTENTIAL).
FT	TRANSMEM 914 939	S6 OF REPEAT 11 (POTENTIAL).
FT	TRANSMEM 1201 1224	S1 OF REPEAT 111 (POTENTIAL).
FT	TRANSMEM 1248 1263	S2 OF REPEAT 111 (POTENTIAL).
FT	TRANSMEM 1270 1291	S3 OF REPEAT 111 (POTENTIAL).
FT	TRANSMEM 1296 1317	S4 OF REPEAT 111 (POTENTIAL).
FT	TRANSMEM 1337 1359	S5 OF REPEAT 111 (POTENTIAL).
FT	TRANSMEM 1444 1470	S6 OF REPEAT 111 (POTENTIAL).
FT	TRANSMEM 1524 1547	S1 OF REPEAT IV (POTENTIAL).
FT	TRANSMEM 1569 1582	S2 OF REPEAT IV (POTENTIAL).
FT	TRANSMEM 1589 1612	S3 OF REPEAT IV (POTENTIAL).
FT	TRANSMEM 1623 1644	S4 OF REPEAT IV (POTENTIAL).
FT	TRANSMEM 1660 1682	S5 OF REPEAT IV (POTENTIAL).
FT	TRANSMEM 1748 1772	S6 OF REPEAT IV (POTENTIAL).
FT	CARBOHYD 214 214	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 283 283	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 288 288	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 291 291	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 318 318	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 328 328	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 548 548	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 592 592	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 740 740	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 803 803	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 841 841	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 864 864	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 946 946	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 1465 1465	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 1374 1374	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 1380 1380	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 1488 1488	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 1746 1746	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 1774 1774	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 1955 1955	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	CARBOHYD 558 558	N-LINKED (GLICNAC - -) (POTENTIAL).
FT	E -> K.	
FT	/FTIDVAR_008955.	

Query Match	Score	DB	Length	GC
Best Local Similarity	60.08			
Matches	67	Conservative	1	Mismatches
			Indels	Errors
QY	1	PSAVATYP	10	
	1	1	1	
DB	1002	PSATATYP	1011	

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Sheet1:comp job id: March 12, 2002, 12:54:41
Job time: 6.06 sec
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/FTIU-VAR_008955.

